c	2	179	83.6	329	50	~~AI682287~~	AI682287 wc51c01.x
c	3	168	78.5	380	36	~~AA631916~~	AA631916 np78b10.s
	4	160	74.8	375	35	~~AA578209~~	AA578209 nl56f11.s
	5	160	74.8	642	48	~~AI557474~~	AI557474 PT2.1_7_G
c	6	142	66.4	322	36	~~AA618586~~	AA618586 np30h03.s
c	7	129	60.3	294	46	~~AI417931~~	AI417931 tg55e07.x
	8	127	59.3	760	48	~~AI557019~~	AI557019 PT2.1_10_
	9	125	58.4	378	39	~~AA876897~~	AA876897 ny47g12.s
c	10	76	35.5	370	63	~~AI972706~~	AI972706 wr42d04.x
	11	53	24.8	545	103	~~AQ503931~~	AQ503931 RPCI-11-3
c	12	20	9.3	276	59	~~AV082866~~	AV082866 AV082866
c	13	19	8.9	421	41	~~AI056551~~	AI056551 oy98d10.x
	14	18	8.4	272	42	~~AI147724~~	AI147724 qb43d09.x
	15	18	8.4	326	28	~~AA081449~~	AA081449 zn06g06.r
	16	18	8.4	522	39	AA835226	AA835226 ak65b06.s
	17	18	8.4	546	47	AI467857	AI467857 tj83g02.x
	18	17	7.9	166	102	AQ346924	AQ346924 RPCI11-11
c	19	17	7.9	268	74	AW208037	AW208037 M111068e
	20	17	7.9	292	43	AI243504	AI243504 qh82a09.x
	[redacted]	17	7.9	299	24	H83957	H83957 ys64h05.s1
		17	7.9	349	74	AV397277	AV397277 AV397277
c	23	17	7.9	386	25	D80092	D80092 HUM027D06B
c	24	17	7.9	391	100	AQ312074	AQ312074 RPCI11-93
	25	17	7.9	402	87	AQ767933	AQ767933 HS_3089_A
c	26	17	7.9	408	105	AQ620046	AQ620046 HS_5186_A
	27	17	7.9	427	88	AQ877464	AQ877464 HS_2146_A
c	28	17	7.9	441	91	AQ145997	AQ145997 HS_2226_A
c	29	17	7.9	443	25	N70966	N70966 za34c02.s1
	30	17	7.9	462	87	AQ815740	AQ815740 HS_5283_B
	31	17	7.9	468	104	AQ555758	AQ555758 HS_5230_B
c	32	17	7.9	484	24	N31364	N31364 yx54g06.r1
	33	17	7.9	485	30	AA197315	AA197315 zq50f03.s
	34	17	7.9	490	43	AI162663	AI162663 A021P32U
	35	17	7.9	506	62	AI903753	AI903753 IL-BT037-
	36	17	7.9	516	22	H11831	H11831 yml1h07.r1
	37	17	7.9	526	100	AQ283408	AQ283408 RPCI11-90
c	38	17	7.9	527	99	AQ234569	AQ234569 HS_2054_A
	39	17	7.9	531	87	AQ805277	AQ805277 HS_3214_A
	40	17	7.9	541	100	AQ313844	AQ313844 RPCI11-94
	41	17	7.9	541	104	AQ563558	AQ563558 HS_5343_A
	42	17	7.9	544	49	AI632528	AI632528 wb10b03.x
	43	17	7.9	546	103	AQ479186	AQ479186 RPCI-11-2
c	44	17	7.9	554	64	AW022746	AW022746 df43a12.y
c	45	17	7.9	566	81	B67277	B67277 T22N3TR TAM

1-14-97

AA081449

11-16-95

ALIGNMENTS

RESULT 1
AI792251
LOCUS AI792251 369 bp mRNA EST 02-JUL-1999
DEFINITION np78b10.y5 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132411 similar to contains Alu repetitive element;contains element MER4 repetitive element ;, mRNA sequence.
ACCESSION AI792251
VERSION AI792251.1 GI:5339967
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 369)
AUTHORS NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jun 5, 1998 this sequence version replaced gi:3187227.
Other_ESTs: np78b10.x5
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation information
This 5' resequenced clone has no previous 5' data to verify this new read against
Putative full length read
The vector to vector length is 370
Seq primer: -40RP from Gibco.

FEATURES Location/Qualifiers
source 1. .369
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1132411"
/clone_lib="NCI_CGAP_Pr2"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected preneoplastic cells histologically-determined to be prostatic intraepithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

BASE COUNT 101 a 88 c 93 g 87 t
ORIGIN

Query Match 99.1%; Score 212; DB 60; Length 369;
Best Local Similarity 100.0%; Pred. No. 7e-107;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       3 AAGGCGTGCAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCCTGCTTGCA 62
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Db       7 AAGGCGTGCAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCCTGCTTGCA 66

Qy      63 AGGTCAGGCAAGCTGGATTCTGGTCCCCACCTTTGCAGAGAGAACAGCGATGTTGTGCGC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 AGGTCAGGCAAGCTGGATTCTGGTCCCCACCTTTGCAGAGAGAACAGCGATGTTGTGCGC 126

Qy     123 CCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTCCAAGAGTGCTTTTCTCTCTAA 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 CCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTCCAAGAGTGCTTTTCTCTCTAA 186

Qy     183 TAAGAAAACATCTACTTTGAAACATCTACTGG 214
          ||||||||||||||||||||||||||||||||
Db     187 TAAGAAAACATCTACTTTGAAACATCTACTGG 218
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RESULT 2
AI682287/c
LOCUS AI682287 329 bp mRNA EST 26-MAY-1999
DEFINITION wc51c01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2322144 3' similar to contains Alu repetitive element;contains element MER4 repetitive element ;, mRNA sequence.
ACCESSION AI682287
VERSION AI682287.1 GI:4892469
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

	2	316	93.2	642	48	AI557474	AI557474 PT2.1_7_G
c	3	292	86.1	329	50	AI682287	AI682287 wc51c01.x
	4	292	86.1	369	60	AI792251	AI792251 np78b10.y
c	5	292	86.1	380	36	AA631916	AA631916 np78b10.s
	6	266	78.5	378	39	AA876897	AA876897 ny47g12.s
c	7	261	77.0	294	46	AI417931	AI417931 tg55e07.x
	8	222	65.5	760	48	AI557019	AI557019 PT2.1_10_
c	9	171	50.4	322	36	AA618586	AA618586 np30h03.s
c	10	76	22.4	370	63	AI972706	AI972706 wr42d04.x
	11	56	16.5	545	103	AQ503931	AQ503931 RPCI-11-3
c	12	34	10.0	531	104	AQ560799	AQ560799 HS_2079_B
	13	30	8.8	417	90	AQ038229	AQ038229 CIT-HSP-2
	14	30	8.8	641	79	AG012358	AG012358 Homo sapi
c	15	30	8.8	645	79	AG012366	AG012366 Homo sapi
	16	30	8.8	652	79	AG012359	AG012359 Homo sapi
	17	30	8.8	725	79	AG012570	AG012570 Homo sapi
c	18	30	8.8	726	79	AG012595	AG012595 Homo sapi
	19	30	8.8	727	79	AG012568	AG012568 Homo sapi
c	20	30	8.8	742	79	AG012593	AG012593 Homo sapi
c	[redacted]	30	8.8	752	79	AG012594	AG012594 Homo sapi
c	[redacted]	29	8.6	390	24	H72049	H72049 yr99b02.s1
c	23	29	8.6	397	36	AA620300	AA620300 af05g04.s
c	24	29	8.6	398	33	AA455041	AA455041 aa04a06.s
c	25	29	8.6	407	24	H73336	H73336 yu05d01.s1
	26	29	8.6	504	82	AQ727006	AQ727006 HS_5431_A
c	27	27	8.0	213	25	N70900	N70900 za33a05.s1
c	28	27	8.0	249	104	AQ586994	AQ586994 RPCI-11-4
c	29	27	8.0	272	21	T92000	T92000 ye01c12.s1
c	30	27	8.0	325	37	AA702361	AA702361 zi87g02.s
c	31	27	8.0	326	21	T96961	T96961 ye50f08.s1
c	32	27	8.0	327	64	AW089007	AW089007 xd34b09.x
c	33	27	8.0	328	35	AA588288	AA588288 no25c12.s
c	34	27	8.0	359	37	AA714684	AA714684 nx91h08.s
c	35	27	8.0	380	34	AA503720	AA503720 ne50f03.s
c	36	27	8.0	383	47	AI500579	AI500579 tn93b04.x
c	37	27	8.0	387	26	W47327	W47327 zc39c12.s1
c	38	27	8.0	390	47	AI522295	AI522295 ti76e03.x
c	39	27	8.0	395	21	R02172	R02172 ye87e07.s1
c	40	27	8.0	396	26	W45269	W45269 zc82e09.s1
c	41	27	8.0	404	21	R01398	R01398 ye77a12.s1
	42	27	8.0	424	26	W47326	W47326 zc39c12.r1
c	43	27	8.0	425	38	AA807307	AA807307 oc38a01.s
	44	27	8.0	427	45	AI349788	AI349788 ta96f08.x
c	45	27	8.0	435	87	AQ757670	AQ757670 HS_2274_B

ALIGNMENTS

RESULT 1
AA578209
LOCUS AA578209 375 bp mRNA EST 12-SEP-1997
DEFINITION nl56f11.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1044717 similar to contains Alu repetitive element;contains element MER4 repetitive element ;, mRNA sequence.
ACCESSION AA578209
VERSION AA578209.1 GI:2356393
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 375)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1407086.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 395 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1044717"
/clone_lib="NCI_CGAP_Pr4"
/sex="male"
/tissue_type="prostatic intraepithelial neoplasia - high grade"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pAMP10; mRNA made from prostate intraepithelial neoplasia (high-grade), cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp.
BASE COUNT 110 a 87 c 90 g 88 t
ORIGIN

Query Match 100.0%; Score 339; DB 35; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.8e-169;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 GACCAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCTTGCTTGCAAGGTC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GACCAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCTTGCTTGCAAGGTC 60

Qy      61 AGGCAAGCTGGATTCTGGTCCCCACCTTTGCAGAGAGAACAGCGATGTTGTGCGCCCATT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGGCAAGCTGGATTCTGGTCCCCACCTTTGCAGAGAGAACAGCGATGTTGTGCGCCCATT 120

Qy     121 TCTCAGATCAAGGACCGGCCCATCTTACTACCTCCAAGAGTGCTTTTCTCTCTAATAAGA 180
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Db     121 TCTCAGATCAAGGACCGGCCCATCTTACTACCTCCAAGAGTGCTTTTCTCTCTAATAAGA 180

Qy     181 AAACATCTACTTTGAAACATCTACTGGGCGAGACCAGGAGTGATGGCTCAGCCTGTAATT 240
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Db     181 AAACATCTACTTTGAAACATCTACTGGGCGAGACCAGGAGTGATGGCTCAGCCTGTAATT 240

Qy     241 CTGGAATTTCGGGAGGCCGAGGCAGGAAGATTCCTTGAGCACAGGAGTTCCAGACCAGCC 300
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Db     241 CTGGAATTTCGGGAGGCCGAGGCAGGAAGATTCCTTGAGCACAGGAGTTCCAGACCAGCC 300

Qy     301 TGGGCAATGTAGCAAGACGCTGTCTCTATTTATACAATA 339
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Db     301 TGGGCAATGTAGCAAGACGCTGTCTCTATTTATACAATA 339
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RESULT 2
AI557474
LOCUS AI557474 642 bp mRNA EST 09-AUG-1999
DEFINITION PT2.1_7_G02.r tumor2 Homo sapiens cDNA 3', mRNA sequence.
ACCESSION AI557474
VERSION AI557474.1 GI:4489837
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 642)
AUTHORS Huang,G.M., Ng,W.l., Farkas,J., He,L., Liang,H.A., Gordon,D., Yu,J. and Hood,L.
TITLE Prostate cancer expression profiling by cDNA sequencing analysis

	2	184	89.8	642	48	~~AI557474~~ AI557474 PT2.1_7_G
c	3	160	78.0	329	50	~~AI682287~~ AI682287 wc51c01.x
	4	160	78.0	369	60	~~AI792251~~ AI792251 np78b10.y
c	5	160	78.0	380	36	~~AA631916~~ AA631916 np78b10.s
	6	134	65.4	378	39	~~AA876897~~ AA876897 ny47g12.s
c	7	131	63.9	322	36	~~AA618586~~ AA618586 np30h03.s
c	8	129	62.9	294	46	~~AI417931~~ AI417931 tg55e07.x
	9	127	62.0	760	48	~~AI557019~~ AI557019 PT2.1_10_
c	10	76	37.1	370	63	~~AI972706~~ AI972706 wr42d04.x
	11	57	27.8	545	103	~~AQ503931~~ AQ503931 RPCI-11-3
c	12	19	9.3	421	41	~~AI056551~~ AI056551 oy98d10.x
	13	18	8.8	272	42	~~AI147724~~ AI147724 qb43d09.x
	14	18	8.8	326	28	AA081449 AA081449 zn06g06.r
	15	18	8.8	522	39	AA835226 AA835226 ak65b06.s
	16	18	8.8	546	47	AI467857 AI467857 tj83g02.x
	17	17	8.3	166	102	AQ346924 AQ346924 RPCI11-11
c	18	17	8.3	268	74	AW208037 AW208037 M111068e
	19	17	8.3	292	43	AI243504 AI243504 qh82a09.x
	20	17	8.3	299	24	H83957 H83957 ys64h05.s1
	21	17	8.3	349	74	AV397277 AV397277 AV397277
c	22	17	8.3	386	25	D80092 D80092 HUM027D06B
c	23	17	8.3	391	100	AQ312074 AQ312074 RPCI11-93
	24	17	8.3	402	87	AQ767933 AQ767933 HS_3089_A
c	25	17	8.3	408	105	AQ620046 AQ620046 HS_5186_A
	26	17	8.3	427	88	AQ877464 AQ877464 HS_2146_A
c	27	17	8.3	441	91	AQ145997 AQ145997 HS_2226_A
c	28	17	8.3	443	25	N70966 N70966 za34c02.s1
	29	17	8.3	462	87	AQ815740 AQ815740 HS_5283_B
	30	17	8.3	468	104	AQ555758 AQ555758 HS_5230_B
c	31	17	8.3	484	24	N31364 N31364 yx54g06.r1
	32	17	8.3	485	30	AA197315 AA197315 zq50f03.s
	33	17	8.3	490	43	AI162663 AI162663 A021P32U
	34	17	8.3	506	62	AI903753 AI903753 IL-BT037-
	35	17	8.3	516	22	H11831 H11831 ym11h07.r1
	36	17	8.3	526	100	AQ283408 AQ283408 RPCI11-90
c	37	17	8.3	527	99	AQ234569 AQ234569 HS_2054_A
	38	17	8.3	541	100	AQ313844 AQ313844 RPCI11-94
	39	17	8.3	541	104	AQ563558 AQ563558 HS_5343_A
	40	17	8.3	544	49	AI632528 AI632528 wb10b03.x
	41	17	8.3	546	103	AQ479186 AQ479186 RPCI-11-2
c	42	17	8.3	554	64	AW022746 AW022746 df43a12.y
c	43	17	8.3	566	81	B67277 B67277 T22N3TR TAM
	44	17	8.3	575	104	AQ507017 AQ507017 RPCI-11-2
	45	17	8.3	579	103	AQ488916 AQ488916 RPCI-11-2

1-14-97 10:20

ALIGNMENTS

ESULT 1
A578209
OCUS AA578209 375 bp mRNA EST 12-SEP-1997
EFINITION n156f11.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1044717 similar to contains Alu repetitive element;contains element MER4 repetitive element ;, mRNA sequence.
CCESSION AA578209
ERSION AA578209.1 GI:2356393
YWORDS EST.
URCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
EFERENCE 1 (bases 1 to 375)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
[redacted] On Sep 12, 1996 this sequence version replaced gi:1407086.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
[redacted]: Robert_Strausberg@nih.gov
[redacted] Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,

cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 395 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.

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FEATURES             Location/Qualifiers
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                     /clone="IMAGE:1044717"
                     /clone_lib="NCI_CGAP_Pr4"
                     /sex="male"
                     /tissue_type="prostatic intraepithelial neoplasia - high
                     grade"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: prostate; Vector: pAMP10; mRNA made from
                     prostate intraepithelial neoplasia (high-grade), cDNA
                     made by oligo-dT priming.  Non-directionally cloned.
                     Size-selected  on agarose gel, average insert size 600 bp.
BASE COUNT      110 a     87 c     90 g     88 t
ORIGIN
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Query Match 99.5%; Score 204; DB 35; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.4e-101;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2 CAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCTTGCTTGCAAGGTCAGG 61
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Db       4 CAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCTTGCTTGCAAGGTCAGG 63

Qy      62 CAAGCTGGATTCTGGTCCCCACCTTTGCAGAGAGAACAGCGATGTTGTGCGCCCATTTCT 121
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Db      64 CAAGCTGGATTCTGGTCCCCACCTTTGCAGAGAGAACAGCGATGTTGTGCGCCCATTTCT 123

Qy     122 CAGATCAAGGACCGGCCCATCTTACTACCTCCAAGAGTGCTTTTCTCTCTAATAAGAAAA 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CAGATCAAGGACCGGCCCATCTTACTACCTCCAAGAGTGCTTTTCTCTCTAATAAGAAAA 183

Qy     182 CATCTACTTTGAAACATCTACTGG 205
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Db     184 CATCTACTTTGAAACATCTACTGG 207
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RESULT   2
AI557474
LOCUS       AI557474      642 bp    mRNA            EST       09-AUG-1999
DEFINITION  PT2.1_7_G02.r tumor2 Homo sapiens cDNA 3', mRNA sequence.
ACCESSION   AI557474
VERSION     AI557474.1  GI:4489837
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 642)
  AUTHORS   Huang,G.M., Ng,W.l., Farkas,J., He,L., Liang,H.A., Gordon,D., Yu,J.
            and Hood,L.
  TITLE     Prostate cancer expression profiling by cDNA sequencing analysis
  JOURNAL   Genomics 59 (2), 178-186 (1999)
  MEDLINE   99339982
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3187163.
            Contact: Guyang Matthew Huang
            Leroy Hood
            University of Washington
            Department of Molecular Biotechnology, Box 357730, University of
            Washington, Seattle, WA 98195
```

c	2	311	89.9	329	50	AI682287	AI682287 wc51c01.x
c	3	300	86.7	380	36	AA631916	AA631916 np78b10.s
	4	292	84.4	375	35	AA578209	AA578209 nl56f11.s
	5	292	84.4	642	48	AI557474	AI557474 PT2.1_7_G
c	6	261	75.4	294	46	AI417931	AI417931 tg55e07.x
	7	257	74.3	378	39	AA876897	AA876897 ny47g12.s
	8	222	64.2	760	48	AI557019	AI557019 PT2.1_10_
	9	182	52.6	322	36	AA618586	AA618586 np30h03.s
c	10	76	22.0	370	63	AI972706	AI972706 wr42d04.x
c	11	53	15.3	545	103	AQ503931	AQ503931 RPCI-11-3
	12	34	9.8	531	104	AQ560799	AQ560799 HS_2079_B
c	13	30	8.7	417	90	AQ038229	AQ038229 CIT-HSP-2
	14	30	8.7	641	79	AG012358	AG012358 Homo sapi
	15	30	8.7	645	79	AG012366	AG012366 Homo sapi
c	16	30	8.7	652	79	AG012359	AG012359 Homo sapi
	17	30	8.7	725	79	AG012570	AG012570 Homo sapi
c	[redacted]	30	8.7	726	79	AG012595	AG012595 Homo sapi
		30	8.7	727	79	AG012568	AG012568 Homo sapi
c	20	30	8.7	742	79	AG012593	AG012593 Homo sapi
c	21	30	8.7	752	79	AG012594	AG012594 Homo sapi
c	22	29	8.4	390	24	H72049	H72049 yr99b02.s1
c	23	29	8.4	397	36	AA620300	AA620300 af05g04.s
c	24	29	8.4	398	33	AA455041	AA455041 aa04a06.s
c	25	29	8.4	407	24	H73336	H73336 yu05d01.s1
	26	29	8.4	504	82	AQ727006	AQ727006 HS_5431_A
c	27	27	7.8	213	25	N70900	N70900 za33a05.s1
c	28	27	7.8	249	104	AQ586994	AQ586994 RPCI-11-4
c	29	27	7.8	272	21	T92000	T92000 ye01c12.s1
c	30	27	7.8	325	37	AA702361	AA702361 zi87g02.s
c	31	27	7.8	326	21	T96961	T96961 ye50f08.s1
c	32	27	7.8	327	64	AW089007	AW089007 xd34b09.x
c	33	27	7.8	328	35	AA588288	AA588288 no25c12.s
c	34	27	7.8	359	37	AA714684	AA714684 nx91h08.s
c	35	27	7.8	380	34	AA503720	AA503720 ne50f03.s
c	36	27	7.8	383	47	AI500579	AI500579 tn93b04.x
c	37	27	7.8	387	26	W47327	W47327 zc39c12.s1
c	38	27	7.8	390	47	AI522295	AI522295 ti76e03.x
c	39	27	7.8	395	21	R02172	R02172 ye87e07.s1
c	40	27	7.8	396	26	W45269	W45269 zc82e09.s1
c	41	27	7.8	404	21	R01398	R01398 ye77a12.s1
	42	27	7.8	424	26	W47326	W47326 zc39c12.r1
c	43	27	7.8	425	38	AA807307	AA807307 oc38a01.s
	44	27	7.8	427	45	AI349788	AI349788 ta96f08.x
c	45	27	7.8	435	87	AQ757670	AQ757670 HS_2274_B

[redacted]

ALIGNMENTS

RESULT 1
AI792251

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LOCUS       AI792251        369 bp    mRNA            EST     02-JUL-1999
DEFINITION  np78b10.y5 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132411
            similar to contains Alu repetitive element;contains element MER4
            repetitive element ;, mRNA sequence.
ACCESSION   AI792251
VERSION     AI792251.1  GI:5339967
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 369)
  AUTHORS   NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Dental Research,
            Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3187227.
            Other_ESTs: np78b10.x5
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
```

M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
information
This 5' resequenced clone has no previous 5' data to verify this
new read against
Putative full length read
The vector to vector length is 370
Seq primer: -40RP from Gibco.

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FEATURES             Location/Qualifiers
     source          1. .369
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1132411"
                     /clone_lib="NCI_CGAP_Pr2"
                     /sex="Male"
                     /dev_stage="45 years old"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; Site_1: NotI; Site_2: EcoRI; 1st
                     strand cDNA was primed with oligo(dT)17 on 50 ng of
                     DNAse-treated, total cellular RNA obtained from
                     5,000-10,000 microdissected preneoplastic cells
                     histologically-determined to be prostatic intraepithelial
                     neoplasia 2 (PIN2) cells.  Double-stranded cDNA was
                     ligated to EcoRI adaptors, 5 cycles of PCR applied to the
                     cDNA with an adaptor-specific primer, and the resulting
                     PCR product subcloned into pAMP10 by the UDG-cloning
                     method (Life Technologies).  Average insert size is 600
                     bp. NOTE: Not directionally cloned.  This library was
                     constructed by  David Krizman."
BASE COUNT      101 a     88 c     93 g     87 t
ORIGIN
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Query Match          99.4%;  Score 344;  DB 60;  Length 369;
Best Local Similarity  100.0%;  Pred. No. 2.5e-172;
Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 AAGGCGTGCAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCCTGCTTGCA 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 AAGGCGTGCAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCCTGCTTGCA 66

Qy      63 AGGTCAGGCAAGCTGGATTCTGGTCCCCACCTTTGCAGAGAGAACAGCGATGTTGTGCGC 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 AGGTCAGGCAAGCTGGATTCTGGTCCCCACCTTTGCAGAGAGAACAGCGATGTTGTGCGC 126

Qy     123 CCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTCCAAGAGTGCTTTTCTCTCTAA 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 CCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTCCAAGAGTGCTTTTCTCTCTAA 186

Qy     183 TAAGAAAACATCTACTTTGAAACATCTACTGGGCGAGACCAGGAGTGATGGCTCAGCCTG 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TAAGAAAACATCTACTTTGAAACATCTACTGGGCGAGACCAGGAGTGATGGCTCAGCCTG 246

Qy     243 TAATTCTGGAATTTCGGGAGGCCGAGGCAGGAAGATTCCTTGAGCACAGGAGTTCCAGAC 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 TAATTCTGGAATTTCGGGAGGCCGAGGCAGGAAGATTCCTTGAGCACAGGAGTTCCAGAC 306

Qy     303 CAGCCTGGGCAATGTAGCAAGACGCTGTCTCTATTTATACAATA 346
           |||||||||||||||||||||||||||||||||||||||||||||
Db     307 CAGCCTGGGCAATGTAGCAAGACGCTGTCTCTATTTATACAATA 350
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RESULT 2
AI682287/c

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LOCUS       AI682287        329 bp    mRNA            EST     26-MAY-1999
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c	2	292	84.4	329	50	AI682287	AI682287 wc51c01.x
	3	292	84.4	375	35	AA578209	AA578209 nl56f11.s
c	4	292	84.4	380	36	AA631916	AA631916 np78b10.s
	5	292	84.4	642	48	AI557474	AI557474 PT2.1_7_G
c	6	261	75.4	294	46	AI417931	AI417931 tg55e07.x
	7	257	74.3	378	39	AA876897	AA876897 ny47g12.s
	8	222	64.2	760	48	AI557019	AI557019 PT2.1_10_
c	9	171	49.4	322	36	AA618586	AA618586 np30h03.s
c	10	76	22.0	370	63	AI972706	AI972706 wr42d04.x
	11	53	15.3	545	103	AQ503931	AQ503931 RPCI-11-3
c	12	34	9.8	531	104	AQ560799	AQ560799 HS_2079_B
	13	30	8.7	417	90	AQ038229	AQ038229 CIT-HSP-2
	14	30	8.7	641	79	AG012358	AG012358 Homo sapi
c	15	30	8.7	645	79	AG012366	AG012366 Homo sapi
	16	30	8.7	652	79	AG012359	AG012359 Homo sapi
	17	30	8.7	725	79	AG012570	AG012570 Homo sapi
c	18	30	8.7	726	79	AG012595	AG012595 Homo sapi
	[redacted]	30	8.7	727	79	AG012568	AG012568 Homo sapi
c		30	8.7	742	79	AG012593	AG012593 Homo sapi
c	21	30	8.7	752	79	AG012594	AG012594 Homo sapi
c	22	29	8.4	390	24	H72049	H72049 yr99b02.s1
c	23	29	8.4	397	36	AA620300	AA620300 af05g04.s
c	24	29	8.4	398	33	AA455041	AA455041 aa04a06.s
c	25	29	8.4	407	24	H73336	H73336 yu05d01.s1
	26	29	8.4	504	82	AQ727006	AQ727006 HS_5431_A
c	27	27	7.8	213	25	N70900	N70900 za33a05.s1
c	28	27	7.8	249	104	AQ586994	AQ586994 RPCI-11-4
c	29	27	7.8	272	21	T92000	T92000 ye01c12.s1
c	30	27	7.8	325	37	AA702361	AA702361 zi87g02.s
c	31	27	7.8	326	21	T96961	T96961 ye50f08.s1
c	32	27	7.8	327	64	AW089007	AW089007 xd34b09.x
c	33	27	7.8	328	35	AA588288	AA588288 no25c12.s
c	34	27	7.8	359	37	AA714684	AA714684 nx91h08.s
c	35	27	7.8	380	34	AA503720	AA503720 ne50f03.s
c	36	27	7.8	383	47	AI500579	AI500579 tn93b04.x
c	37	27	7.8	387	26	W47327	W47327 zc39c12.s1
c	38	27	7.8	390	47	AI522295	AI522295 ti76e03.x
c	39	27	7.8	395	21	R02172	R02172 ye87e07.s1
c	40	27	7.8	396	26	W45269	W45269 zc82e09.s1
c	41	27	7.8	404	21	R01398	R01398 ye77a12.s1
	42	27	7.8	424	26	W47326	W47326 zc39c12.r1
c	43	27	7.8	425	38	AA807307	AA807307 oc38a01.s
	44	27	7.8	427	45	AI349788	AI349788 ta96f08.x
c	45	27	7.8	435	87	AQ757670	AQ757670 HS_2274_B

01-2-95

ALIGNMENTS

RESULT 1
AI792251
LOCUS AI792251 369 bp mRNA EST 02-JUL-1999
DEFINITION np78b10.y5 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132411 similar to contains Alu repetitive element;contains element MER4 repetitive element ;, mRNA sequence.
ACCESSION AI792251
VERSION AI792251.1 GI:5339967
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 369)
AUTHORS NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jun 5, 1998 this sequence version replaced gi:3187227.
Other_ESTs: np78b10.x5
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation information
This 5' resequenced clone has no previous 5' data to verify this new read against
Putative full length read
The vector to vector length is 370
Seq primer: -40RP from Gibco.

FEATURES Location/Qualifiers
source 1..369
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1132411"
/clone_lib="NCI_CGAP_Pr2"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected preneoplastic cells histologically-determined to be prostatic intraepithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

BASE COUNT 101 a 88 c 93 g 87 t
ORIGIN

Query Match 84.7%; Score 293; DB 60; Length 369;
Best Local Similarity 99.7%; Pred. No. 2e-145;
Matches 343; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3 AAGGCGTGCAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCYTGCTTGCA 62
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       7 AAGGCGTGCAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCCTGCTTGCA 66

Qy      63 AGGTCAGGCAAGCTGGATTCTGGTCCCCACCTTTGCAGAGAGAACAGCGATGTTGTGCGC 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 AGGTCAGGCAAGCTGGATTCTGGTCCCCACCTTTGCAGAGAGAACAGCGATGTTGTGCGC 126

Qy     123 CCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTCCAAGAGTGCTTTTCTCTCTAA 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 CCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTCCAAGAGTGCTTTTCTCTCTAA 186

Qy     183 TAAGAAAACATCTACTTTGAAACATCTACTGGGCGAGACCAGGAGTGATGGCTCAGCCTG 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TAAGAAAACATCTACTTTGAAACATCTACTGGGCGAGACCAGGAGTGATGGCTCAGCCTG 246

Qy     243 TAATTCTGGAATTTCGGGAGGCCGAGGCAGGAAGATTCCTTGAGCACAGGAGTTCCAGAC 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 TAATTCTGGAATTTCGGGAGGCCGAGGCAGGAAGATTCCTTGAGCACAGGAGTTCCAGAC 306

Qy     303 CAGCCTGGGCAATGTAGCAAGACGCTGTCTCTATTTATACAATA 346
           ||||||||||||||||||||||||||||||||||||||||||||
Db     307 CAGCCTGGGCAATGTAGCAAGACGCTGTCTCTATTTATACAATA 350
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RESULT 2
AI682287/c
LOCUS AI682287 329 bp mRNA EST 26-MAY-1999

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VERSION     T83743.1  GI:712031
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 387)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 742
            High quality sequence stops: 258 Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 742   Std Error: 0.00
            Seq primer: T3
            High quality sequence stop: 258.
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                     /db_xref="taxon:9606"
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                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      129 a     70 c     76 g    106 t      6 others
ORIGIN

al[redacted]nt_scores:
            Quality:   77.00             Length:     45
              Ratio:  2.406               Gaps:      1
 Percent Similarity:  71.111   Percent Identity: 40.000

alignment_block:
 US-09-065-672-12 x T83743   ..

 Align seg 1/1  to: T83743  from: 1  to: 387

      12 AlaHisLeuThrThrSerLysSerAlaPheLeuSerAsnLysLysThrSe 28
         |||   |||:::::::::|||:::      |||:::|||:::|||:::
      10 GCGCTACTGAGCAGTGATAAACAAAAGGTATTGAATAATGAAAAATCAAT 59

      28 rThrLeuLysHisLeuLeuGlyGluThrArgSerAspGlySerAlaCysA 45
            |||                 :::|||   :::|||||||:::||||
      60 CATCCTG.................GCCAGGCACAGTGGCTCATGCTGTA 91

      45 snSerGlyIleSerGlyGlyArgGlyArgLysIle 56
         ||:::::|||   |||||||:::|||||||:::|||
      92 ATTNCAGCATTTTGGGAGGCCAAGGTAGGAGGATC 126

seq_name: gb_est16:AA570478
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seq_documentation_block:
LOCUS       AA570478      495 bp    mRNA            EST       25-AUG-1997
DEFINITION  nk64a02.s1 NCI_CGAP_Sch1 Homo sapiens cDNA clone IMAGE:1018250 3'
            similar to contains Alu repetitive element;, mRNA sequence.
ACCESSION   AA570478
VERSION     AA570478.1  GI:2344458
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 495)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 8, 1995 this sequence version replaced gi:801198.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
            Ph.D.
            cDNA Library Arraying: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 440.
FEATURES             Location/Qualifiers
     source          1. .495
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                     /clone="IMAGE:1018250"
                     /clone_lib="NCI_CGAP_Sch1"
                     /tissue_type="Schwannoma tumor"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; Cloned unidirectionally.  Primer: Oligo dT. Two
                     pooled bulk Schwannoma tumors. 5' adaptor sequence: 5'
                     GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTT 3' Average insert size:  1.2 kb."
BASE COUNT      134 a    129 c    114 g    118 t
ORIGIN

alignment_scores:
            Quality:   76.50             Length:     50
              Ratio:  2.250               Gaps:      2
 Percent Similarity:  68.000   Percent Identity: 40.000

alignment_block:
 US-09-065-672-12 x AA570478/rev   ..

 Align seg 1/1  to reverse of: AA570478  from: 1  to: 495

      10 GlyProAlaHisLeuThrThrSerLysSerAlaPheLeuSerAsnLysLy 26
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     227 GGATCGCCTGAGGTCAGGAGTTCGAGATCAGCCTGGCTAACATGTCGAAG 178

      26 sThrSerThrLeuLys......HisLeuLeuGlyGluThrArgSerAspG 41
         :   |||   ||||||         |||   |||:::          :
     177 CCCCTCTTTACTAAAAATACAAAAATTAGCCGGGCAT.........GGTG 137

      41 lySerAlaCysAsnSerGlyIleSerGlyGlyArgGlyArgLysIlePro 57
         :::::|||||:::   :::   |||||||||||||||||:::||||||
     136 CAGGCGCCTGTGATCCCAGCTACTCAGGAGGCCGAGGCAGAAGAATCCCT 87

seq_name: gb_gss14:AQ553229
```

```
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1397868.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Insert Length: 424    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .322
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1117877"
                     /clone_lib="NCI_CGAP_Pr22"
                     /sex="male"
                     /tissue_type="normal prostate"
                     /lab_host="DH10B"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; 1st strand cDNA was prepared
                     from normal prostate bulk tissue, and was then primed with
                     a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I  and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized, and was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       80 a      77 c      76 g      89 t
ORIGIN


alignment_scores:
            Quality:   137.00              Length:      26
              Ratio:   5.269                 Gaps:       0
 Percent Similarity:   100.000   Percent Identity:  100.000

alignment_block:
 US-09-065-672-13 x AA618586/rev    ..

 Align seg 1/1  to reverse of: AA618586  from: 1  to: 322

       1 MetLeuCysAlaHisPheSerAspGlnGlyProAlaHisLeuThrThrSe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     254 ATGTTGTGCGCCCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTC 205

      17 rLysSerAlaPheLeuSerAsnLysLys 26
         ||||||||||||||||||||||||||||
     204 CAAGAGTGCTTTTCTCTCTAATAAAAAA 177

seq_name: gb_est4:R94063

seq_documentation_block:
LOCUS       R94063         277 bp    mRNA            EST       22-JAN-1999
DEFINITION  yt74a08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:275991 3', mRNA sequence.
ACCESSION   R94063
VERSION     R94063.1  GI:969458
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1  (bases 1 to 277)
            Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837823.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 909
            High quality sequence stops: 204
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 909    Std Error: 0.00
            Seq primer: Promega -21m13
            High quality sequence stop: 204.
FEATURES             Location/Qualifiers
     source          1. .277
                     /organism="Homo sapiens"
                     /db_xref="GDB:3799604"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:275991"
                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT       88 a      54 c      43 g      80 t      12 others
ORIGIN


alignment_scores:
            Quality:    58.00              Length:      22
              Ratio:   3.412                 Gaps:       0
 Percent Similarity:   77.273   Percent Identity:  50.000

alignment_block:
 US-09-065-672-13 x R94063    ..

 Align seg 1/1  to: R94063  from: 1  to: 277

       5 HisPheSerAspGlnGlyProAlaHisLeuThrThrSerLysSerAlaPh 21
         ||||||::::::::::   |||   |||   ||||||:::   |||:::
      29 CATTTTACAGAAAGGGAACCATAACATTACACAACAAAGTNTAGCTGTAA 78

      21 eLeuSerAsnLysLys 26
         :::||||||||||||
      79 AATCTCAAATAAGAAA 94

seq_name: gb_est6:N74923

seq_documentation_block:
LOCUS       N74923         261 bp    mRNA            EST       29-MAR-1996
DEFINITION  za45d03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:295493 3', mRNA sequence.
ACCESSION   N74923
VERSION     N74923.1  GI:1237469
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
```

(1026) Public Availability Genbank 9-1-95

Published 4-5-1996 (1026)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 261)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT On May 18, 1995 this sequence version replaced gi:811191.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
High quality sequence stop: 239.
FEATURES Location/Qualifiers
source 1. .261
/organism="Homo sapiens"
/db_xref="GDB:1240414"
/db_xref="taxon:9606"
/clone="IMAGE:295493"
/clone_lib="Soares fetal liver spleen 1NFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 101 a 50 c 37 g 72 t 1 others
ORIGIN

alignment_scores:
Quality: 57.00 Length: 22
Ratio: 3.353 Gaps: 0
Percent Similarity: 77.273 Percent Identity: 50.000

alignment_block:
US-09-065-672-13 x N74923 ..

Align seg 1/1 to: N74923 from: 1 to: 261

```
      5 HisPheSerAspGlnGlyProAlaHisLeuThrThrSerLysSerAlaPh 21
        ||||||:::::::::   |||   |||   |||||||:::   |||:::
     38 CATTTTACAGAAAGGGAACCATAACATTACACAACAAAGTATAGCTGTAA 87

     21 eLeuSerAsnLysLys 26
        :::|||||||||||||
     88 AATCTCAAATAAGAAA 103
```

seq_name: gb_est12:AA280704

seq_documentation_block:
LOCUS AA280704 306 bp mRNA EST 14-AUG-1997
DEFINITION zs96g03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711508 3', mRNA sequence.
ACCESSION AA280704
VERSION AA280704.1 GI:1923401
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Pub Avail 3-3-97 102(a)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 306)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1394868.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham.
FEATURES Location/Qualifiers
source 1. .306
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:711508"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 97 a 44 c 56 g 109 t
ORIGIN

alignment_scores:
Quality: 57.00 Length: 22
Ratio: 3.353 Gaps: 0
Percent Similarity: 77.273 Percent Identity: 50.000

alignment_block:
US-09-065-672-13 x AA280704/rev ..

Align seg 1/1 to reverse of: AA280704 from: 1 to: 306

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      5 HisPheSerAspGlnGlyProAlaHisLeuThrThrSerLysSerAlaPh 21
        ||||||:::::::::   |||   |||   |||||||:::   |||:::
    251 CATTTTACAGAAAGGGAACCATAACATTACACAACAAAGTATAGCTGTAA 202

     21 eLeuSerAsnLysLys 26
        :::|||||||||||||
    201 AATCTCAAATAAGAAA 186
```

seq_name: gb_est1:Z39296

seq_documentation_block:
LOCUS Z39296 331 bp mRNA EST 31-OCT-1994
DEFINITION HSC16F052 normalized infant brain cDNA Homo sapiens cDNA clone c-16f05 3', mRNA sequence.
ACCESSION Z39296
VERSION Z39296.1 GI:562488
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Pub Avail 10-27-94

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 331)
AUTHORS Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,

```
            Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
            Sebastiani-Kabaktchis,C. and Tessier,A.
  TITLE     IMAGE: molecular integration of the analysis of the human genome
            and its expression
  JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
  MEDLINE   95277534
COMMENT     Contact: Genethon
            Genexpress-Genethon
            Genethon Centre de recherche sur le Genome Humain
            1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
            Tel: 33169472800
            Fax: 33160778698
            Email: genexpress@genethon.fr
            Single read. 22 T removed at sequence 5'end
            Genexpress_library_idt: C; Genexpress_sequence_idt: a1c-16f05
            Seq primer: (-21)M13_universal.
FEATURES              Location/Qualifiers
     source           1. .331
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="c-16f05"
                      /clone_lib="normalized infant brain cDNA"
                      /sex="Female"
                      /tissue_type="total brain"
                      /dev_stage="3 months old"
                      /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
                      Site_2: NotI; sex=Female; dev_stage=3 months old;
                      isolate=muscular atrophy patient;  tissue_type=total
                      brain;  total mRNA was oligo-(dT) primed and directionally
                      cloned 5' -> 3' into the  HindIII -> NotI sites of the
                      lafmid BA vector. Clone library from B.Soares,  Psychiatry
                      Dept. Columbia University, USA.  Normalization_method:
                      Bento Soares, P.N.A.S in press"
BASE COUNT       129 a      61 c      47 g      91 t       3 others
ORIGIN


alignment_scores:
            Quality:   57.00              Length:     22
              Ratio:   3.353                Gaps:      0
 Percent Similarity:   77.273   Percent Identity: 50.000

alignment_block:
 US-09-065-672-13 x Z39296    ..

 Align seg 1/1  to: Z39296  from: 1  to: 331

       5 HisPheSerAspGlnGlyProAlaHisLeuThrThrSerLysSerAlaPh 21
         ||||||:::::::::   |||   |||   |||||||:::   |||:::
      38 CATTTTACAGAAAGGGAACCATAACATTACACAACAAAGTATAGCTGTAA 87

      21 eLeuSerAsnLysLys 26
         :::|||||||||||||
      88 AATCTCAAATAAGAAA 103

seq_name: gb_est22:AI023420

seq_documentation_block:
LOCUS       AI023420      340 bp    mRNA            EST       28-AUG-1998
DEFINITION  ow71g05.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:1652312 3', mRNA sequence.
ACCESSION   AI023420
VERSION     AI023420.1  GI:3239826
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
```

6-19-98

```
COMMENT     On Jan 9, 1998 this sequence version replaced gi:937906.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 911    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 332.
FEATURES              Location/Qualifiers
     source           1. .340
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1652312"
                      /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                      /sex="male"
                      /dev_stage="20 week-post conception fetus"
                      /lab_host="DH10B (ampicillin resistant)"
                      /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                      with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                      This is a subtracted version of the original Soares fetal
                      liver spleen 1NFLS library.  1st strand cDNA was primed
                      with a Pac I - oligo(dT) primer [5'
                      AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Pac I and cloned into the Pac I
                      and Eco RI sites of the modified pT7T3 vector.  Library
                      went through one round of normalization. Library
                      constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT       130 a      60 c      48 g     102 t
ORIGIN


alignment_scores:
            Quality:   57.00              Length:     22
              Ratio:   3.353                Gaps:      0
 Percent Similarity:   77.273   Percent Identity: 50.000

alignment_block:
 US-09-065-672-13 x AI023420    ..

 Align seg 1/1  to: AI023420  from: 1  to: 340

       5 HisPheSerAspGlnGlyProAlaHisLeuThrThrSerLysSerAlaPh 21
         ||||||:::::::::   |||   |||   |||||||:::   |||:::
      52 CATTTTACAGAAAGGGAACCATAACATTACACAACAAAGTATAGCTGTAA 101

      21 eLeuSerAsnLysLys 26
         :::|||||||||||||
     102 AATCTCAAATAAGAAA 117
```

```
            Japan 305
            Tel: 0298-38-7441
            Fax: 0298-38-7468
            Email: tsasaki@abr.affrc.go.jp.
FEATURES              Location/Qualifiers
     source           1. .460
                      /organism="Oryza sativa"
                      /cultivar="Nipponbare"
                      /db_xref="taxon:4530"
                      /clone="C12371_1A"
                      /clone_lib="Rice callus cDNA"
                      /tissue_type="callus"
                      /dev_stage="callus"
BASE COUNT      151 a      74 c     174 g      56 t       5 others
ORIGIN


alignment_scores:
            Quality:   61.50              Length:      25
              Ratio:  3.075                Gaps:       1
 Percent Similarity:  80.000   Percent Identity: 56.000

alignment_block:
 US-09-065-672-14 x C26462    ..

 Align seg 1/1  to: C26462  from: 1  to: 460

       6 LeuGlyGluThrArgSerAspGlySerAla.........CysAsnSerGl 19
         ||||||||||:::||||||   :::||||||          |||::::::
      23 CTTGGTGAGAATCGATCAAAGAGCAGTGCCAGCTGCAGCTGCAGCANGAG 72

      19 yIleSerGlyGlyArgGlyArgLys 27
          |||:::||||||||||||||||:::
      73 GATCGGAGGAGGAAGGGGGAGAAGA 97

seq_name: gb_est6:N80180

seq_documentation_block:
LOCUS       N80180         334 bp    mRNA            EST       29-MAR-1996
DEFINITION  za65h07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:297469 3' similar to contains Alu repetitive element;, mRNA
            sequence.
ACCESSION   N80180
VERSION     N80180.1  GI:1242881
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:785498.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: m13 -40 forward
            High quality sequence stop: 157.
FEATURES              Location/Qualifiers
     source           1. .334
                      /organism="Homo sapiens"
                      /db_xref="GDB:1242390"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:297469"
                      /clone_lib="Soares fetal liver spleen 1NFLS"
                      /sex="male"
                      /dev_stage="20 week-post conception fetus"
                      /lab_host="DH10B (ampicillin resistant)"
                      /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                      with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                      1st strand cDNA was primed with a Pac I - oligo(dT) primer
                      [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Pac I and cloned into the Pac I
                      and Eco RI sites of the modified pT7T3 vector.  Library
                      went through one round of normalization. Library
                      constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT       63 a      82 c      82 g     106 t       1 others
ORIGIN


alignment_scores:
            Quality:   60.50              Length:      26
              Ratio:  3.184                Gaps:       1
 Percent Similarity:  73.077   Percent Identity: 57.692

alignment_block:
 US-09-065-672-14 x N80180/rev    ..

 Align seg 1/1  to reverse of: N80180  from: 1  to: 334

       2 LeuLysHisLeuLeuGlyGluThrArgSerAspGlySerAlaCysAsnSe 18
         ||||||      :::   ::::::||||||   |||   |||||||||
     168 CTAAAAATACAAATATTAGATGTGCGTAGTGCGGGC...GCCTGTAATCC 122

      18 rGlyIleSerGlyGlyArgGlyArgLys 27
          :::   ||||||||||||||||||||
     121 CAGCTACTCAGGAGGCAGAGGCAGGAAA 94
```

4-4-96

	2	316	93.2	642	48	AI557474 PT2.1_7_G
c	3	292	86.1	329	50	AI682287 wc51c01.x
	4	292	86.1	369	60	AI792251 np78b10.y
c	5	292	86.1	380	36	AA631916 np78b10.s
	6	266	78.5	378	39	AA876897 ny47g12.s
c	7	261	77.0	294	46	AI417931 tg55e07.x
	8	222	65.5	760	48	AI557019 PT2.1_10_
c	9	171	50.4	322	36	AA618586 np30h03.s
c	10	76	22.4	370	63	AI972706 wr42d04.x
	11	56	16.5	545	103	AQ503931 RPCI-11-3
c	12	34	10.0	531	104	AQ560799 HS_2079_B
	13	30	8.8	417	90	AQ038229 CIT-HSP-2
	14	30	8.8	641	79	AG012358 Homo sapi
c	15	30	8.8	645	79	AG012366 Homo sapi
	16	30	8.8	652	79	AG012359 Homo sapi
	17	30	8.8	725	79	AG012570 Homo sapi
c	18	30	8.8	726	79	AG012595 Homo sapi
	19	30	8.8	727	79	AG012568 Homo sapi
c	20	30	8.8	742	79	AG012593 Homo sapi
[redacted]	21	30	8.8	752	79	AG012594 Homo sapi
	22	29	8.6	390	24	H72049 yr99b02.s1
c	23	29	8.6	397	36	AA620300 af05g04.s
c	24	29	8.6	398	33	AA455041 aa04a06.s
c	25	29	8.6	407	24	H73336 yu05d01.s1
	26	29	8.6	504	82	AQ727006 HS_5431_A
c	27	27	8.0	213	25	N70900 za33a05.s1
c	28	27	8.0	249	104	AQ586994 RPCI-11-4
c	29	27	8.0	272	21	T92000 ye01c12.s1
c	30	27	8.0	325	37	AA702361 zi87g02.s
c	31	27	8.0	326	21	T96961 ye50f08.s1
c	32	27	8.0	327	64	AW089007 xd34b09.x
c	33	27	8.0	328	35	AA588288 no25c12.s
c	34	27	8.0	359	37	AA714684 nx91h08.s
c	35	27	8.0	380	34	AA503720 ne50f03.s
c	36	27	8.0	383	47	AI500579 tn93b04.x
c	37	27	8.0	387	26	W47327 zc39c12.s1
c	38	27	8.0	390	47	AI522295 ti76e03.x
c	39	27	8.0	395	21	R02172 ye87e07.s1
c	40	27	8.0	396	26	W45269 zc82e09.s1
c	41	27	8.0	404	21	R01398 ye77a12.s1
	42	27	8.0	424	26	W47326 zc39c12.r1
c	43	27	8.0	425	38	AA807307 oc38a01.s
	44	27	8.0	427	45	AI349788 ta96f08.x
c	45	27	8.0	435	87	AQ757670 HS_2274_B

11-2-99

ALIGNMENTS

RESULT 1
AA578209
LOCUS AA578209 375 bp mRNA EST 12-SEP-1997
DEFINITION nl56f11.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1044717 similar to contains Alu repetitive element;contains element MER4 repetitive element ;, mRNA sequence.
ACCESSION AA578209
VERSION AA578209.1 GI:2356393
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 375)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1407086.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 395 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
FEATURES Location/Qualifiers
source 1. .375
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1044717"
/clone_lib="NCI_CGAP_Pr4"
/sex="male"
/tissue_type="prostatic intraepithelial neoplasia - high grade"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pAMP10; mRNA made from prostate intraepithelial neoplasia (high-grade), cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp."
BASE COUNT 110 a 87 c 90 g 88 t
ORIGIN

Query Match 100.0%; Score 339; DB 35; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.8e-169;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 GACCAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCTTGCTTGCAAGGTC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GACCAAACAGAGCGCCACTGGGAGGCTGAAACCTTTAGGCCGATGCTTGCTTGCAAGGTC 60

Qy      61 AGGCAAGCTGGATTCTGGTCCCCACCTTTGCAGAGAGAACAGCGATGTTGTGCGCCCATT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGGCAAGCTGGATTCTGGTCCCCACCTTTGCAGAGAGAACAGCGATGTTGTGCGCCCATT 120

Qy     121 TCTCAGATCAAGGACCGGCCCATCTTACTACCTCCAAGAGTGCTTTTCTCTCTAATAAGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TCTCAGATCAAGGACCGGCCCATCTTACTACCTCCAAGAGTGCTTTTCTCTCTAATAAGA 180

Qy     181 AAACATCTACTTTGAAACATCTACTGGGCGAGACCAGGAGTGATGGCTCAGCCTGTAATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AAACATCTACTTTGAAACATCTACTGGGCGAGACCAGGAGTGATGGCTCAGCCTGTAATT 240

Qy     241 CTGGAATTTCGGGAGGCCGAGGCAGGAAGATTCCTTGAGCACAGGAGTTCCAGACCAGCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGGAATTTCGGGAGGCCGAGGCAGGAAGATTCCTTGAGCACAGGAGTTCCAGACCAGCC 300

Qy     301 TGGGCAATGTAGCAAGACGCTGTCTCTATTTATACAATA 339
          |||||||||||||||||||||||||||||||||||||||
Db     301 TGGGCAATGTAGCAAGACGCTGTCTCTATTTATACAATA 339
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RESULT 2
AI557474
LOCUS AI557474 642 bp mRNA EST 09-AUG-1999
DEFINITION PT2.1_7_G02.r tumor2 Homo sapiens cDNA 3', mRNA sequence.
ACCESSION AI557474
VERSION AI557474.1 GI:4489837
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 642)
AUTHORS Huang,G.M., Ng,W.l., Farkas,J., He,L., Liang,H.A., Gordon,D., Yu,J. and Hood,L.
TITLE Prostate cancer expression profiling by cDNA sequencing analysis

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 376.

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FEATURES             Location/Qualifiers
     source          1. .378
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1274950"
                     /clone_lib="NCI_CGAP_Pr12"
                     /sex="male"
                     /tissue_type="metastatic prostate bone lesion"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from metastatic prostate
                     lesion of the bone, cDNA made by  oligo-dT priming.
                     Non-directionally cloned.  Size-selected on agarose  gel,
                     average insert size 600 bp.  Library made by D. Krizman,
                     NIH."
BASE COUNT      106 a     89 c     94 g     89 t
ORIGIN
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alignment_scores:
            Quality:  298.00            Length:     57
              Ratio:  5.228               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-065-672-12 x AA876897   ..

 Align seg 1/1  to: AA876897  from: 1  to: 378

       1 MetLeuCysAlaHisPheSerAspGlnGlyProAlaHisLeuThrThrSe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     120 ATGTTGTGCGCCCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTC 169

      17 rLysSerAlaPheLeuSerAsnLysLysThrSerThrLeuLysHisLeuL 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     170 CAAGAGTGCTTTTCTCTCTAATAAGAAAACATCTACTTTGAAACATCTAC 219

      34 euGlyGluThrArgSerAspGlySerAlaCysAsnSerGlyIleSerGly 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     220 TGGGCGAGACCAGGAGTGATGGCTCAGCCTGTAATTCTGGAATTTCGGGA 269

      51 GlyArgGlyArgLysIlePro 57
         |||||||||||||||||||||
     270 GGCCGAGGCAGGAAGATTCCT 290
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seq_name: gb_est17:AA631916

seq_documentation_block:
LOCUS        AA631916 102w 380 bp    mRNA            EST       30-OCT-1997
DEFINITION   np78b10.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132411
             similar to contains Alu repetitive element;contains element MER4
             repetitive element ;, mRNA sequence.
ACCESSION    AA631916
VERSION      AA631916.1  GI:2554527
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 380)
  AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
  JOURNAL    Unpublished (1997)
  COMMENT    On Sep 12, 1996 this sequence version replaced gi:1406914.
             Contact: Robert Strausberg, Ph.D.
             Tel: (301) 496-1550
```

Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 470 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.

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FEATURES             Location/Qualifiers
     source          1. .380
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1132411"
                     /clone_lib="NCI_CGAP_Pr2"
                     /sex="Male"
                     /dev_stage="45 years old"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st
                     strand cDNA was primed with oligo(dT)17 on 50 ng of
                     DNAse-treated, total cellular RNA obtained from
                     5,000-10,000 microdissected preneoplastic cells
                     histologically-determined to be prostatic intraepithelial
                     neoplasia 2 (PIN2) cells.  Double-stranded cDNA was
                     ligated to EcoRI adaptors, 5 cycles of PCR applied to the
                     cDNA with an adaptor-specific primer, and the resulting
                     PCR product subcloned into pAMP10 by the UDG-cloning
                     method (Life Technologies).  Average insert size is 600
                     bp. NOTE: Not directionally cloned.  This library was
                     constructed by  David Krizman."
BASE COUNT       87 a     92 c     90 g    111 t
ORIGIN
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alignment_scores:
            Quality:  298.00            Length:     57
              Ratio:  5.228               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-065-672-12 x AA631916/rev   ..

 Align seg 1/1  to reverse of: AA631916  from: 1  to: 380

       1 MetLeuCysAlaHisPheSerAspGlnGlyProAlaHisLeuThrThrSe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     264 ATGTTGTGCGCCCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTC 215

      17 rLysSerAlaPheLeuSerAsnLysLysThrSerThrLeuLysHisLeuL 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     214 CAAGAGTGCTTTTCTCTCTAATAAGAAAACATCTACTTTGAAACATCTAC 165

      34 euGlyGluThrArgSerAspGlySerAlaCysAsnSerGlyIleSerGly 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     164 TGGGCGAGACCAGGAGTGATGGCTCAGCCTGTAATTCTGGAATTTCGGGA 115

      51 GlyArgGlyArgLysIlePro 57
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     114 GGCCGAGGCAGGAAGATTCCT 94
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seq_name: gb_est29:AI557474

seq_documentation_block:
LOCUS        AI557474      642 bp    mRNA            EST       09-AUG-1999
DEFINITION   PT2.1_7_G02.r tumor2 Homo sapiens cDNA 3', mRNA sequence.
ACCESSION    AI557474
VERSION      AI557474.1  GI:4489837
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-065-672-13 x AI792251   ..

 Align seg 1/1  to: AI792251  from: 1  to: 369

       1 MetLeuCysAlaHisPheSerAspGlnGlyProAlaHisLeuThrThrSe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     116 ATGTTGTGCGCCCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTC 165

      17 rLysSerAlaPheLeuSerAsnLysLysThrSer 28
         ||||||||||||||||||||||||||||||||
     166 CAAGAGTGCTTTTCTCTCTAATAAGAAAACATCT 199

seq_name: gb_est37:AI972706

seq_documentation_block:
LOCUS       AI972706      370 bp    mRNA            EST       25-AUG-1999
DEFINITION  wr42d04.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2490343 3'
            similar to contains Alu repetitive element;contains element MER4
            repetitive element ;, mRNA sequence.
ACCESSION   AI972706
VERSION     AI972706.1  GI:5769532
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 370)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Dec 20, 1995 this sequence version replaced gi:1135022.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .370
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2490343"
                     /clone_lib="NCI_CGAP_Pr28"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI_CGAP_Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     985608-986759, 1101192-1101959, and 1217928-1220615).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT       86 a     78 c     76 g    130 t
ORIGIN


alignment_scores:
            Quality:  146.00            Length:     28
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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-065-672-13 x AI972706/rev   ..

 Align seg 1/1  to reverse of: AI972706  from: 1  to: 370

       1 MetLeuCysAlaHisPheSerAspGlnGlyProAlaHisLeuThrThrSe 17
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     286 ATGTTGTGCGCCCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTC 237

      17 rLysSerAlaPheLeuSerAsnLysLysThrSer 28
         ||||||||||||||||||||||||||||||||
     236 CAAGAGTGCTTTTCTCTCTAATAAAAAAACATCT 203

seq_name: gb_est16:AA578209

seq_documentation_block:
LOCUS       AA578209      375 bp    mRNA            EST       12-SEP-1997
DEFINITION  nl56f11.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1044717
            similar to contains Alu repetitive element;contains element MER4
            repetitive element ;, mRNA sequence.
ACCESSION   AA578209
VERSION     AA578209.1  GI:2356393
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 375)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407086.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,
            M.D., Michael R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Insert Length: 395   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .375
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1044717"
                     /clone_lib="NCI_CGAP_Pr4"
                     /sex="male"
                     /tissue_type="prostatic intraepithelial neoplasia - high
                     grade"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: prostate; Vector: pAMP10; mRNA made from
                     prostate intraepithelial neoplasia (high-grade), cDNA
                     made by oligo-dT priming.  Non-directionally cloned.
                     Size-selected  on agarose gel, average insert size 600 bp.
                      "
BASE COUNT      110 a     87 c     90 g     88 t
ORIGIN


alignment_scores:
            Quality:  146.00            Length:     28
              Ratio:  5.214               Gaps:      0
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alignment_block:
 US-09-065-672-13 x AA578209    ..

 Align seg 1/1  to: AA578209  from: 1  to: 375

       1 MetLeuCysAlaHisPheSerAspGlnGlyProAlaHisLeuThrThrSe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     105 ATGTTGTGCGCCCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTC 154

      17 rLysSerAlaPheLeuSerAsnLysLysThrSer 28
         ||||||||||||||||||||||||||||||||||
     155 CAAGAGTGCTTTTCTCTCTAATAAGAAAACATCT 188

seq_name: gb_est20:AA876897

seq_documentation_block:
LOCUS       AA876897      378 bp    mRNA            EST       25-MAR-1998
DEFINITION  ny47g12.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1274950
            similar to contains Alu repetitive element;contains element LTR3
            repetitive element ;, mRNA sequence.
ACCESSION   AA876897
VERSION     AA876897.1  GI:2985974
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 378)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Feb 13, 1998 this sequence version replaced gi:2761085.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
            Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 376.
FEATURES              Location/Qualifiers
     source           1. .378
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1274950"
                      /clone_lib="NCI_CGAP_Pr12"
                      /sex="male"
                      /tissue_type="metastatic prostate bone lesion"
                      /lab_host="DH10B"
                      /note="Vector: pAMP10; mRNA made from metastatic prostate
                      lesion of the bone, cDNA made by  oligo-dT priming.
                      Non-directionally cloned.  Size-selected on agarose  gel,
                      average insert size 600 bp.  Library made by D. Krizman,
                      NIH."
BASE COUNT      105 a     89 c     94 g     89 t
ORIGIN


alignment_scores:
            Quality:  146.00            Length:     28
              Ratio:  5.214               Gaps:      0
ent Similarity: 100.000   Percent Identity: 100.000

lock:
-13 x AA876897    ..
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 Align seg 1/1  to: AA876897  from: 1  to: 378

       1 MetLeuCysAlaHisPheSerAspGlnGlyProAlaHisLeuThrThrSe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     120 ATGTTGTGCGCCCATTTCTCAGATCAAGGACCGGCCCATCTTACTACCTC 169

      17 rLysSerAlaPheLeuSerAsnLysLysThrSer 28
         ||||||||||||||||||||||||||||||||||
     170 CAAGAGTGCTTTTCTCTCTAATAAGAAAACATCT 203

seq_name: gb_est17:AA631916

seq_documentation_block:
LOCUS       AA631916      380 bp    mRNA            EST       30-OCT-1997
DEFINITION  np78b10.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132411
            similar to contains Alu repetitive element;contains element MER4
            repetitive element ;, mRNA sequence.
ACCESSION   AA631916
VERSION     AA631916.1  GI:2554527                                  10-31-97
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 380)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1406914.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
            M.D., Michael Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Insert Length: 470   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES              Location/Qualifiers
     source           1. .380
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1132411"
                      /clone_lib="NCI_CGAP_Pr2"
                      /sex="Male"
                      /dev_stage="45 years old"
                      /lab_host="DH10B"
                      /note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st
                      strand cDNA was primed with oligo(dT)17 on 50 ng of
                      DNAse-treated, total cellular RNA obtained from
                      5,000-10,000 microdissected preneoplastic cells
                      histologically-determined to be prostatic intraepithelial
                      neoplasia 2 (PIN2) cells.  Double-stranded cDNA was
                      ligated to EcoRI adaptors, 5 cycles of PCR applied to the
                      cDNA with an adaptor-specific primer, and the resulting
                      PCR product subcloned into pAMP10 by the UDG-cloning
                      method (Life Technologies).  Average insert size is 600
                      bp. NOTE: Not directionally cloned.  This library was
                      constructed by  David Krizman."
BASE COUNT       87 a     92 c     90 g    111 t
ORIGIN


alignment_scores:
            Quality:  146.00            Length:     28
              Ratio:  5.214               Gaps:      0
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      17 nSerGlyIleSerGlyGlyArgGlyArgLys 27
         ||||||||||||||||||||||||||||||
     119 TTCTGGAATTTCGGGAGGCCGAGGCAGGAAG 89

seq_name: gb_est34:AI792251

seq_documentation_block:
LOCUS       AI792251      369 bp    mRNA            EST       02-JUL-1999
DEFINITION  np78b10.y5 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132411
            similar to contains Alu repetitive element;contains element MER4
            repetitive element ;, mRNA sequence.
ACCESSION   AI792251
VERSION     AI792251.1  GI:5339967
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 369)
  AUTHORS   NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Dental Research,
            Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3187227.
            Other_ESTs: np78b10.x5
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
            M.D., Michael Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            This read is a RESEQUENCE of a previously sequenced human clone
            Original clone citation: see original entry for original citation
            information
            This 5' resequenced clone has no previous 5' data to verify this
            new read against
            Putative full length read
            The vector to vector length is 370
            Seq primer: -40RP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .369
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1132411"
                      /clone_lib="NCI_CGAP_Pr2"
                      /sex="Male"
                      /dev_stage="45 years old"
                      /lab_host="DH10B"
                      /note="Vector: pAMP10; Site_1: NotI; Site_2: EcoRI; 1st
                      strand cDNA was primed with oligo(dT)17 on 50 ng of
                      DNAse-treated, total cellular RNA obtained from
                      5,000-10,000 microdissected preneoplastic cells
                      histologically-determined to be prostatic intraepithelial
                      neoplasia 2 (PIN2) cells.  Double-stranded cDNA was
                      ligated to EcoRI adaptors, 5 cycles of PCR applied to the
                      cDNA with an adaptor-specific primer, and the resulting
                      PCR product subcloned into pAMP10 by the UDG-cloning
                      method (Life Technologies).  Average insert size is 600
                      bp. NOTE: Not directionally cloned.  This library was
                      constructed by  David Krizman."
BASE COUNT      101 a     88 c     93 g     87 t
ORIGIN

alignment_scores:
           Quality:  141.00            Length:     27
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-065-672-14 x AI792251   ..

 Align seg 1/1  to: AI792251  from: 1  to: 369

       1 ThrLeuLysHisLeuLeuGlyGluThrArgSerAspGlySerAlaCysAs 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     200 ACTTTGAAACATCTACTGGGCGAGACCAGGAGTGATGGCTCAGCCTGTAA 249

      17 nSerGlyIleSerGlyGlyArgGlyArgLys 27
         ||||||||||||||||||||||||||||||
     250 TTCTGGAATTTCGGGAGGCCGAGGCAGGAAG 280

seq_name: gb_est16:AA578209

seq_documentation_block:
LOCUS       AA578209      375 bp    mRNA            EST       12-SEP-1997
DEFINITION  nl56f11.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1044717
            similar to contains Alu repetitive element;contains element MER4
            repetitive element ;, mRNA sequence.
ACCESSION   AA578209
VERSION     AA578209.1  GI:2356393
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 375)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407086.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,
            M.D., Michael R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Insert Length: 395   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES              Location/Qualifiers
     source           1. .375
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1044717"
                      /clone_lib="NCI_CGAP_Pr4"
                      /sex="male"
                      /tissue_type="prostatic intraepithelial neoplasia - high
                      grade"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /note="Organ: prostate; Vector: pAMP10; mRNA made from
                      prostate intraepithelial neoplasia (high-grade), cDNA
                      made by oligo-dT priming.  Non-directionally cloned.
                      Size-selected  on agarose gel, average insert size 600 bp.
                      "
BASE COUNT      110 a     87 c     90 g     88 t
ORIGIN

alignment_scores:
           Quality:  141.00            Length:     27
             Ratio:  5.222               Gaps:      0
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alignment_block:
 US-09-065-672-14 x AA578209    ..

 Align seg 1/1  to: AA578209  from: 1  to: 375

       1 ThrLeuLysHisLeuLeuGlyGluThrArgSerAspGlySerAlaCysAs 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     189 ACTTTGAAACATCTACTGGGCGAGACCAGGAGTGATGGCTCAGCCTGTAA 238

      17 nSerGlyIleSerGlyGlyArgGlyArgLys 27
         ||||||||||||||||||||||||||||||
     239 TTCTGGAATTTCGGGAGGCCGAGGCAGGAAG 269

seq_name: gb_est20:AA876897

seq_documentation_block:
LOCUS        AA876897      378 bp    mRNA            EST       25-MAR-1998
DEFINITION   ny47g12.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1274950
             similar to contains Alu repetitive element;contains element LTR3
             repetitive element ;, mRNA sequence.
ACCESSION    AA876897
VERSION      AA876897.1  GI:2985974
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 378)
  AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
  JOURNAL    Unpublished (1997)
COMMENT      On Feb 13, 1998 this sequence version replaced gi:2761085.
             Contact: Robert Strausberg, Ph.D.
             Tel: (301) 496-1550
             Email: Robert_Strausberg@nih.gov
             Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
             Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
              cDNA Library Preparation: David B. Krizman, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html

             Seq primer: -40m13 fwd. ET from Amersham
             High quality sequence stop: 376.
FEATURES             Location/Qualifiers
     source          1. .378
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1274950"
                     /clone_lib="NCI_CGAP_Pr12"
                     /sex="male"
                     /tissue_type="metastatic prostate bone lesion"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from metastatic prostate
                     lesion of the bone, cDNA made by  oligo-dT priming.
                     Non-directionally cloned.  Size-selected on agarose  gel,
                     average insert size 600 bp.  Library made by D. Krizman,
                     NIH."
BASE COUNT      106 a     89 c     94 g     89 t
ORIGIN


alignment_scores:
            Quality:  141.00            Length:     27
              Ratio:  5.222               Gaps:      0
 t Similarity: 100.000   Percent Identity: 100.000

 ock:
 14 x AA876897    ..
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 Align seg 1/1  to: AA876897  from: 1  to: 378

       1 ThrLeuLysHisLeuLeuGlyGluThrArgSerAspGlySerAlaCysAs 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     204 ACTTTGAAACATCTACTGGGCGAGACCAGGAGTGATGGCTCAGCCTGTAA 253

      17 nSerGlyIleSerGlyGlyArgGlyArgLys 27
         ||||||||||||||||||||||||||||||
     254 TTCTGGAATTTCGGGAGGCCGAGGCAGGAAG 284

seq_name: gb_est17:AA631916

seq_documentation_block:
LOCUS        AA631916      380 bp    mRNA            EST       30-OCT-1997
DEFINITION   np78b10.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132411
             similar to contains Alu repetitive element;contains element MER4
             repetitive element ;, mRNA sequence.
ACCESSION    AA631916
VERSION      AA631916.1  GI:2554527
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 380)
  AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
  JOURNAL    Unpublished (1997)
COMMENT      On Sep 12, 1996 this sequence version replaced gi:1406914.
             Contact: Robert Strausberg, Ph.D.
             Tel: (301) 496-1550
             Email: Robert_Strausberg@nih.gov
             Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
             M.D., Michael Emmert-Buck, M.D., Ph.D.
              cDNA Library Preparation: David B. Krizman, Ph.D.
              cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html

             Insert Length: 470   Std Error: 0.00
             Seq primer: -40m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .380
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1132411"
                     /clone_lib="NCI_CGAP_Pr2"
                     /sex="Male"
                     /dev_stage="45 years old"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st
                     strand cDNA was primed with oligo(dT)17 on 50 ng of
                     DNAse-treated, total cellular RNA obtained from
                     5,000-10,000 microdissected preneoplastic cells
                     histologically-determined to be prostatic intraepithelial
                     neoplasia 2 (PIN2) cells.  Double-stranded cDNA was
                     ligated to EcoRI adaptors, 5 cycles of PCR applied to the
                     cDNA with an adaptor-specific primer, and the resulting
                     PCR product subcloned into pAMP10 by the UDG-cloning
                     method (Life Technologies).  Average insert size is 600
                     bp. NOTE: Not directionally cloned.  This library was
                     constructed by  David Krizman."
BASE COUNT      87 a     92 c     90 g    111 t
ORIGIN


alignment_scores:
            Quality:  141.00            Length:     27
              Ratio:  5.222               Gaps:      0
```